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INTRODUCTION TO THE SYMPOSIUM: "THE NEW MORPHOLOGY: POTENTIAL FOR INTEGRATING NEW TECHNIQUES AND CONCEPTS"

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First, I want to thank the National Science Foundation Visiting Professorships for Women Program and the Mellon Foundation Programs. They are responsible for my being in California at my host institution, California Institute of Technology, and for contacts with Rancho Santa Ana Botanic Garden. They have facilitated my introduction to what is happening in the fields of molecular genetics, imaging procedures, computer technology, as well as a number of other disciplines, which are making important and exciting impacts on developmental and evolutionary biology. The Mellon Foundation also facilitated my interaction with RSABG, because Michael Donoghue as well as Geeta Bharathan, who is one of the speakers today, were Mellon Fellows in my laboratory at the Smithsonian. The Mellon Foundation also provides funds for some of the students in the graduate program at RSABG, where I got to know Mark Porter. Mark and I arrived in southern California at the same time, and we have been trying to initiate formal cooperation between RSABG and Cal Tech on some projects. The Cal Tech connection, continuing from Roy Taylor's mention (Taylor 1996), is further enhanced by George Beadle who worked there and was an early investigator of the evolution of maize from teosinte. This is the focus of John Doebley's research program about which you will hear later (Doebley 1996)

Second, I want to thank the Staff at RSABG, in particular Ann Joslin, and the students who have been working to bring this program together. It is particularly challenging because we are audiotaping the contributions, supplementing the talk by Andres Collazo with a video, and plan to publish the proceedings in RSABG's journal *Aliso*. I have put together a bibliography that will lead you to some of the literature pertinent to the syntheses presented here. You will hear from a number of young speakers. Certainly speakers who are on the rise in their careers—a good sign of an exciting symposium. This reminds me of the period during which I was a Postdoctoral Fellow and had the opportunity, thanks to Jim Estes, to organize a symposium for AIBS, sponsored by the American Society for Plant Taxonomy at Pennsylvania State University. I had been learning about cladistics at a workshop sponsored by Tom Duncan at Berkeley as well as plant molecular biology in Virginia Walbot's laboratory at Stanford University. Also, I was doing genetics while looking at comparative studies of maize evolution. At the time, I was trying to bring molecular biology techniques into systematic studies in plants, and to learn something of where these could be applied. This symposium was very important. Certainly it was the first where many taxonomists heard about the kind of work Jeff Palmer, then at the Carnegie Institution Plant Biology laboratory at Stanford, was initiating at that time. It had a lot of repercussions in the field of plant taxonomy.

When I was teaching biochemistry at Louisiana State University, among the things I emphasized to my students was that in certain instances technology often either leads a field in new directions or creates new interdisciplinary programs. I would talk about how protein purification, electron microscopy, and cell fractionation pushed biochemistry into the prominence it reached in the fifties. Such progress moved forward in the seventies and eighties with all the new DNA technologies. These advances have had a large impact on evolutionary biology since the eighties. I personally was a beneficiary of one technique, PCR (Polymerase Chain Reaction®). This procedure has made DNA studies accessible to museums, such as the Smithsonian Institution, as well as to other institutions as botanic gardens, which have invested in molecular genetics. In my postdoc days, thanks to interaction with Rob DeSalle, a graduate student at that time, I became well informed on the literature and potential interface between genetics and development, and how these could illuminate evolutionary studies. I was interested in the idea of getting training in the field, should I be so lucky as to have a sabbatical. At the time, I actually thought that at first I would be forced into a Drosophila laboratory for such a sabbatical.

Fortunately, I encountered Elliot Meyerowitz at the 1987 Botanical Congress. He had been implementing a program to bring *Arabidopsis* into the model-system realm for plant scientists. He began by telling me about some exciting double mutants and I realized that Elliot not only worked on Drosophila but also worked on plants. Here was a great opportunity! You will hear more in the keynote talk this evening (which is not published, but see the Literature Cited and Pertinent References).

Elliot, Sue Wessler, and Mike Freeling, about three years ago, put together an exciting symposium at Taos, New Mexico, on evolution and development. At least one of the speakers, Cynthia Jones, is here today because of that symposium (Jones and Price 1996). I met her there and learned what she was doing. John Doebley, whom I actually met in my postdoc days, did for me what probably was the most flattering thing that could happen. He called me thinking that I had a post doc available; actually, I was a post doc at that time. Major Goodman had misinformed him about my status in life. Thus, we have kept in touch over the years because of our common interest in maize.

Today a number of themes will be developed; certainly, questions will arise that I would like you to think about as you listen to the talks. We will get back to these during the discussion session at the end. I have outlined some of the points for you to think about as you learn some of the new technologies, or the old technologies applied in different ways. Think about which approaches might show the best potential for applications to studies of systematics in plant and animal diversity. Major issues here, both an historical issue and a continuing philosophical and practical issue, are the definitions of homology and strategies for homologizing characters. You will see significant emphasis on homology considerations in the talks, starting with an introduction by Andres Collazo. Subsequently you will hear new methods and concepts that will allow us to get better assessments for detecting both genetic and developmental redundancies. We will have to think about means of dealing with these as we relate them to evolutionary studies, particularly in developing phylogenies. Throughout the talks, think about where you see these methodologies and conceptual themes going and where they might impact. I think they might impact a diversity of fields including paleobiology, physiology, and ecology. Meanwhile, developmental biologists who have produced the new methodologies and concepts will gain reciprocal illumination for their work from organismal biologists who begin using these advances, Zimmer (1994).

Some of you who are used to the regular RSABG symposia might wonder why the beginning and ending talks are by zoologists. One of the many things I learned as a post doc was how useful it is to be aware of what is going on in other fields and to talk regularly with people using other kinds of model systems and other ways of looking at problems. Also, some of the techniques used by botanists were first developed using animal systems. We continually find that there is not as much dialogue or enough awareness of the literature between botanists and zoologists as you might think. John Doebley has done some exciting work on quantitative genetics and on morphological transitions from teosinte to maize. On the way to these meetings, I was reading a review article in *Current Biology* outlining Charles Langely's work on bristles in flies (Langely 1995). There is a commonality in what he is finding. But no references to the plant world. This is something that could be a topic of discussion.

Do we need more model systems in order to understand character evolution? One thing that has been discussed is the utility, and the possible tractability, of developing systems for studies on land plants that can be informative for phylogenetic studies. Another issue that I think may be a good jumping-off place for discussion is to look at the importance and the frequency of quantitative characters versus discrete characters, and how tractable they are for use in phylogenetics. Where can these best inform and improve our understanding of adaptive evolution?

And now, I am pleased to present the first of the papers today that will present some of the exciting new techniques that are being used in plant and animal system studies.

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